A   SEQ ID NO. 7

```
caggcggcgagatgaggcgggcgccagcgtttctgagcgccgacgaggtgcaggaccacc -  60
------------------------------------------------------------
tccgcagctccagcctcctcatcccgcccctggaggccgcactggccaacttctccaaag - 120
------------------------------------------------------------
gtcccgacggaggggtcatgcaaccggtgcgcaccgtggtgcctgtggccaagcaccgag - 180
------------------------------------------------------------
gcttcttgggagtcatgccagcctacagtgccgctgaggatgcactcaccaccaagttag - 240
------------------------------------------------------------
tcaccttctatgagggccacagcaacaatgctgtcccctcccaccaggcatcagtgcttc - 300
------------------------------------------------------------
tctttgatcccagcaatggttccctgctggcggtcatggatggaaatgtcataactgcaa - 360
------------------------------------------------------------
agaggacagcagccgtctctgccatcgccaccaagttttttgaagcccccaggcagtgatg - 420
------------------------------------------------------------
tgctgtgcattcttggggctggggtccaggcgtacagtcactatgagatcttcacagaac - 480
------------------------------------------------------------
agttctccttcaaggaggtgagaatgtggaaccgcaccagggaaatgctgagaagtttg - 540
------------------------------------------------------------
caagctcagtgcagggagatgttcgggtctgttcatcagtgcaggaggctgtgacaggtg - 600
------------a-----------------------------------------------
ccgatgtcatcatcacagtcaccatggcaacggagcccattttatttggtgaatgggtga - 660
------------------------------------------g-----------------
agcccgggggctcacatcaatgctgttggagccagtagacctgactggcgagaactggatg - 720
--------a---------------------------------------------------
acgagctcatgaagcaagcagtgctgtatgtggactcccgggaggctgccctaaaggagt - 780
---------------------t--------------------------------------
caggagatgttctgttgtcaggggctgacatctttgctgagcttggagaagtggtttcag - 840
------------------------------------------------------------
gagcgaagcctgcatactgtgagaagaccacggtgttcaagtctttggggatggcagtgg - 900
------------------------------------------------------------
aggacctggtcgcagccaaattagtgtacgattcgtggtcatctggcaagtgagcagaag - 960
--------------------------------------------------
gagctgtgcctgggctggatggacgtcacggctcaaacgctggctcagtgtctagatcaa -1020
------------a-----------------------------------------------
aggaggcctagtccccagtgaacgggagtgagagtcactcataagtattgacatccctat -1080
------------------------------------------------------------
tcatgtttgtggttggata                                          -1099
-------------------
```

B

```
Rat      1 MRRAPAFLSADEVQDHLRSSSLLIPPLEAALANFSKGPDGGVMQPVRTVVPVAKHRGFLG   (SEQ ID NO.8)
Mouse    1 -K--------E-------------------------------------------------   (SEQ ID NO.9)
Human    1 -S-V------A-EE--------------T------S-E--------------T----Y--   (SEQ ID. NO.10)


Rat     61 VMPAYSAAEDALTTKLVTFYEG* HSNNAVPSHQASVLLFDPSNGSLLAVMDGNVITAKRT
Mouse   61 ---------------------*---T----------------------------------
Human   61 ---------------------DRGITSV------T----E----T---------------


Rat    120 AAVSAIATKFLKPPGSDVLCILGAGVQAYSHYEIFTEQFSFKEVRMWNRTRENAEKFASS
Mouse  120 ---------L-------------------------------------------------T
Human  121 --------------S-E-------------------------I----K------DT


Rat    180 VQGDVRVCSSVQEAVTGADVIITVTMATEPILFGEWVKPGAHINAVGASRPDWRELDDEL
Mouse  180 ------------------------------------------------------------
Human  181 ---E-----------A---------L----------------------------------


Rat    240 MKQAVLYVDSREAALKESGDVLLSGADIFAELGEVVSGAKPAYCEKTTVFKSLGMAVEDL
Mouse  240 -R-------------------------------I------H------------------
Human  241 -E--------Q---------------E--------IK-V---H----------------T


Rat    300 VAAKLVYDSWSSGK
Mouse  300 --------------
Human  301 -----I--------
```
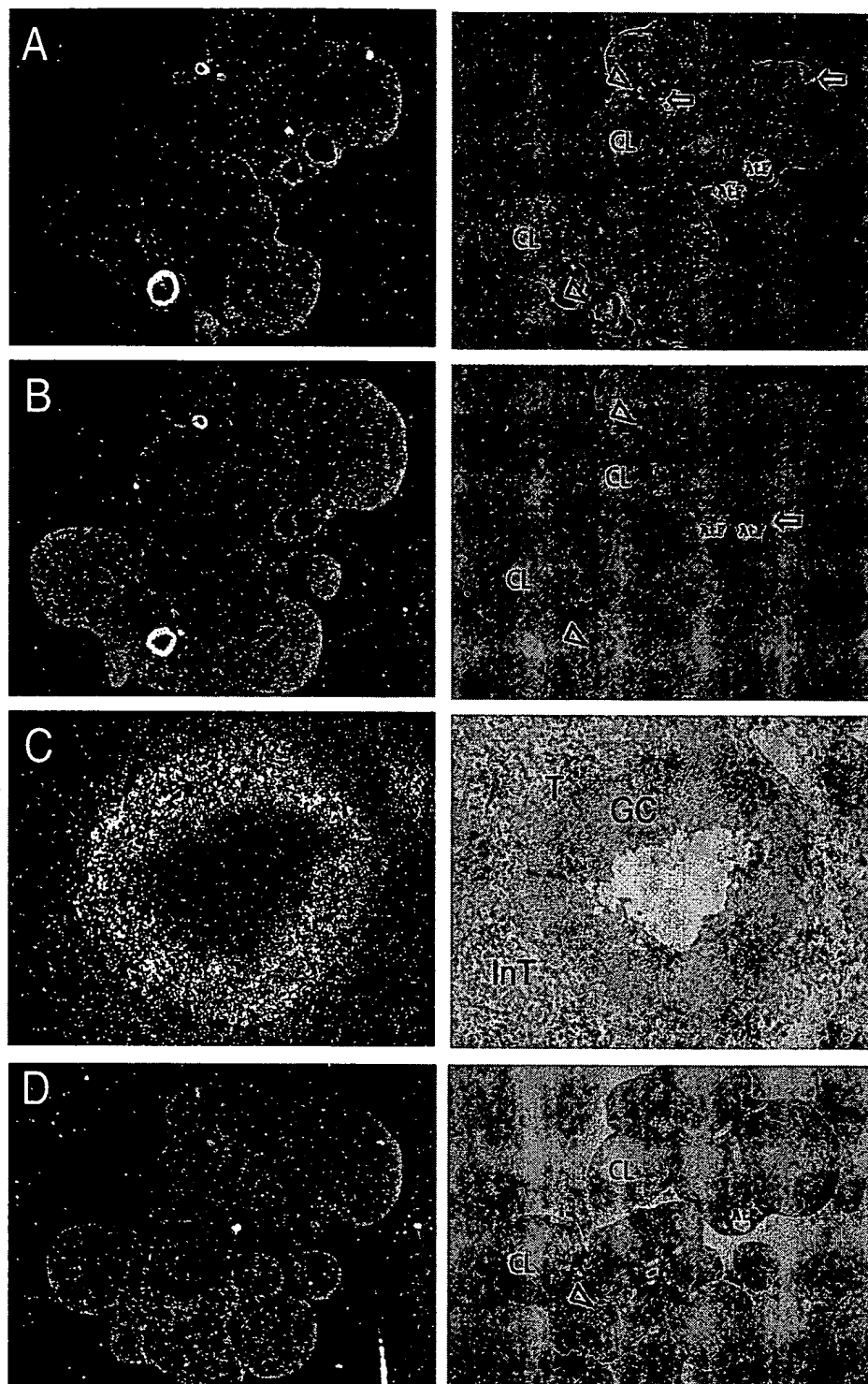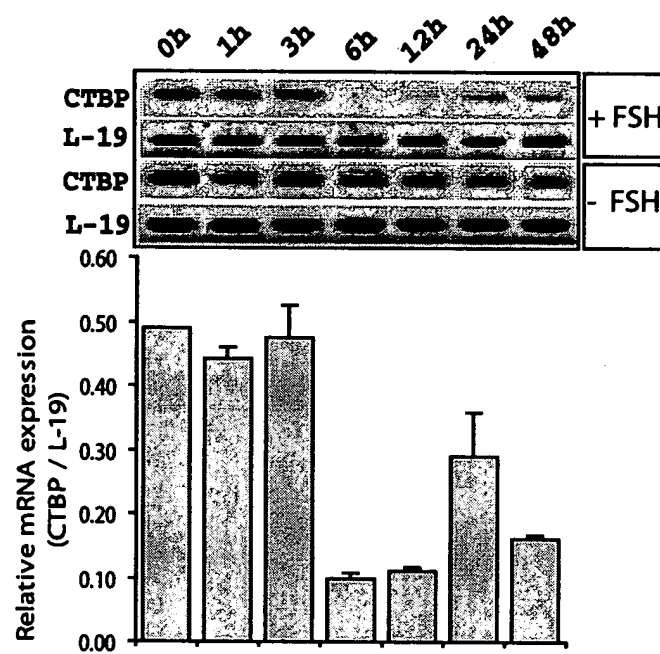
FIG.1.

FIG.2

A

B

FIG.3
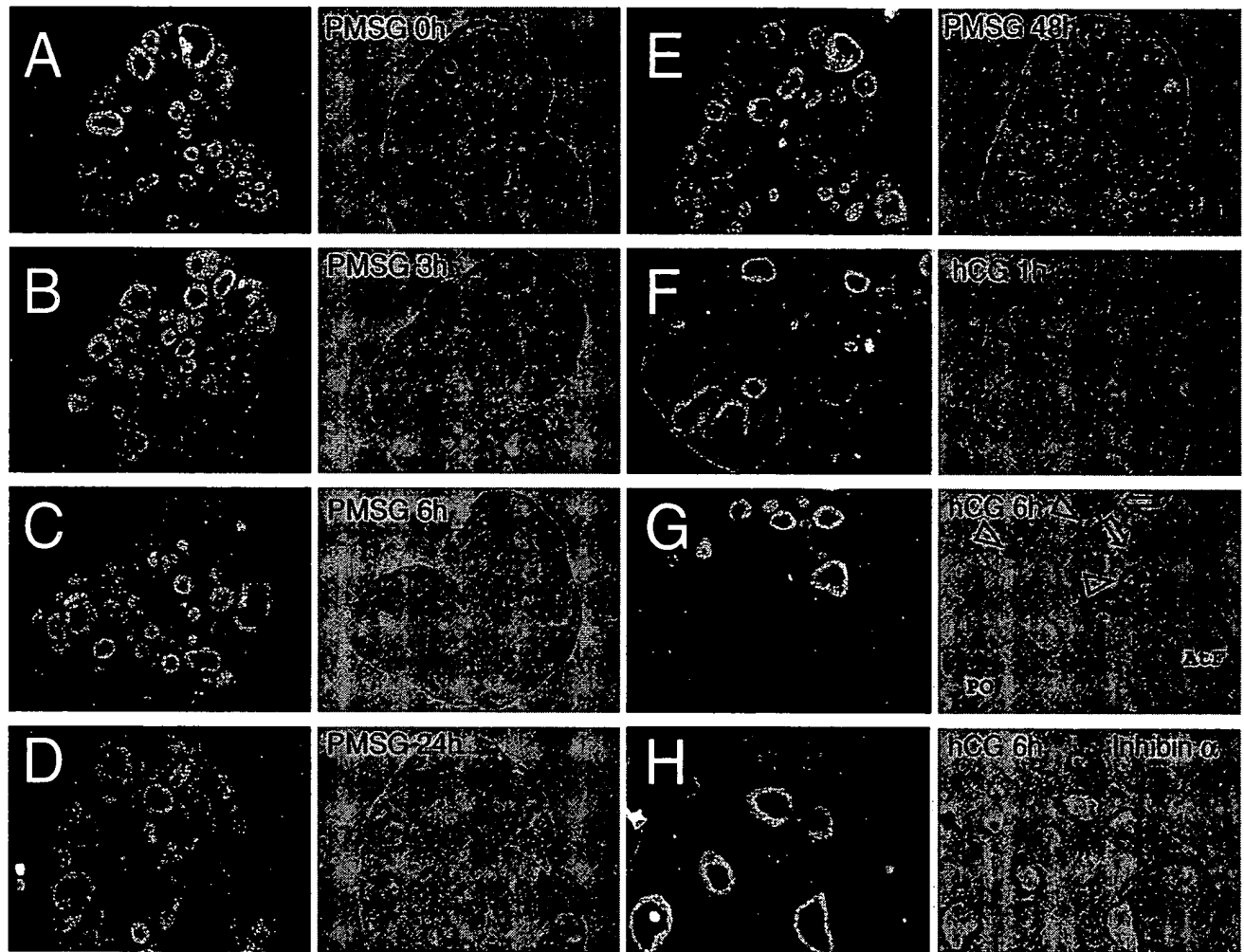
FIG.4
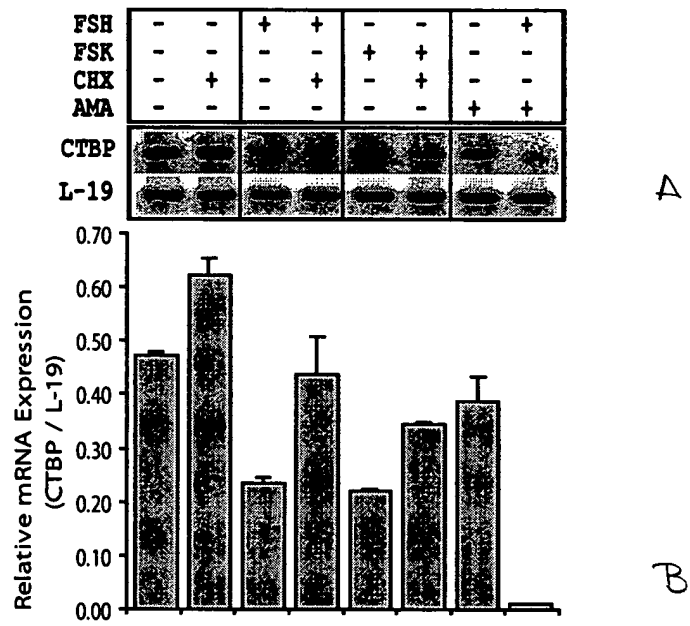
FIG. 5
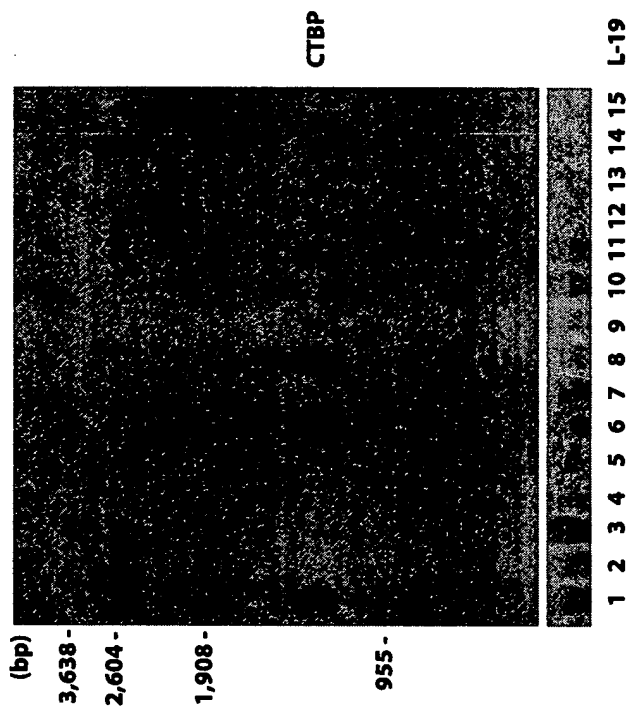
FIG.6

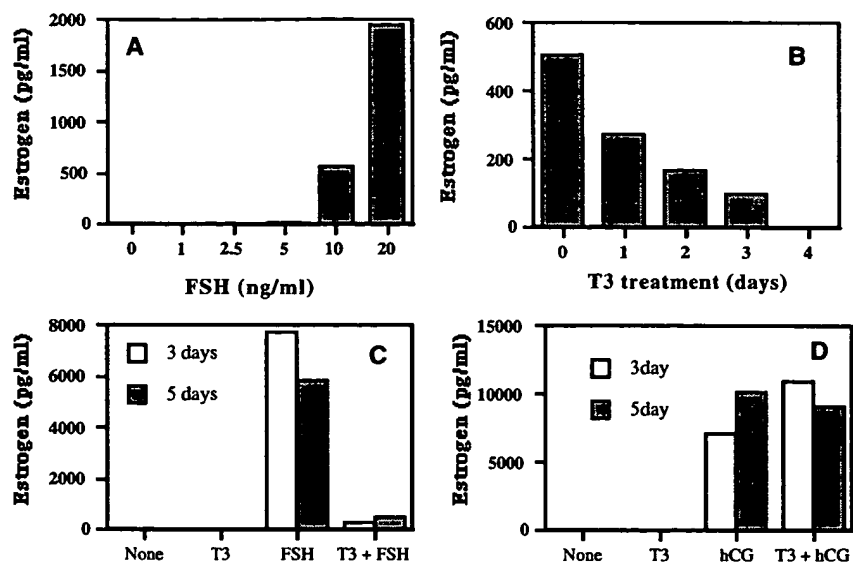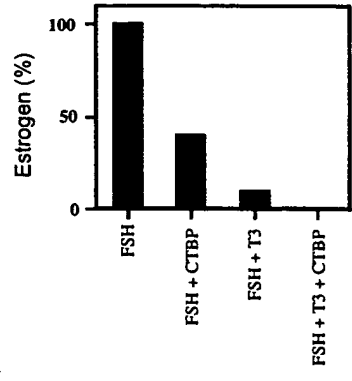Fig. 7

Fig. 8

Fig. 9

(A) DNA sequence: SEQ I D NO. 11

```
  1 gtggcgagca ggaaaaatgg cggccgggtt caaaactgtg gaaccgctgg agtattacag
 61 gagatttctg aaagaaaact gccgtccaga tggaagagaa cttggtgaat tcagaaccac
121 aactgtcaac ataggttcga tcagtacagc ggatggctct gctctagtga agctgggggaa
181 caccacagtc atttgtggag ttaaagcaga atttgcagca ccaccagtag atgcccctga
241 tagaggatat gtcgtcccta atgtggacct accaccgctg tgttcatcga ggtttcggac
301 tggacctcct ggagaagagg ctcaagtaac cagccagttc attgcagatg tcattgagaa
361 ctcacacata attaagaaag aggacttatg catttctcca gggaagcttg ctgggttct
421 atactgtgac cttatttgcc tagactacga tgggaacatt ttggatgcct gcacatttgc
481 tttgttagca gctttaaaga atgtacagtt gcctgaagtt actataaatg aagaaactgc
541 tttagcggaa gtcaatttaa agaagaaaag ttatttgaat gttagagcaa acccagttgc
601 tacttcattt gctgtgtttg atgacacttt gctgatagtc gatcctaccg gggaggaggg
661 gcaccctgtc cacaggaacc ttaaccgtag taatggacga ggaaggcaag ctgtgctgtc
721 ttcacaagcc aggtggggagt gggctgctgg agctaaactt caggactgca tgagtcgagc
781 agtaacgaga cacaaagaag tgagcaaact actggatgaa gtaattcaga gcatgaaaca
841 caaatgaaca gacgccacga ttgtaaaaca gctgtaaaaa ttgtatttgt tacactgtgc
901 acaggccttt tatactaaat aaatacctaa ttcattctt tgaaaaaaaa aaaaaaaaa
961 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
```
• Start codon and stop codon are indicated by bold letters

(B) Protein sequence: SEQ ID. NO. 12

MAAGFKTVEPLEYYRRFLKENCRPDGRELGEFRTTTVNIGSISTADGSALVKLGNTTVICGVKAEFAAP
PVDAPDRGYVVPNVDLPPLCSSRFRTGPPGEEAQVTSQFIADVIENSHIIKKEDLCISPGKLAWVLYCDL
ICLDYDGNILDACTFALLAALKNVQLPEVTINEETALAEVNLKKKSYLNVRANPVATSFAVFDDTLLIV
DPTGEEGHPVHRNLNRSNGRGRQAVLSSQARWEWAAGAKLQDCMSRAVTRHKEVSKLLDEVIQSM
KHK

(C) open reading frame: SEQ ID NO. 13

```
                            1 gtggcgagcaggaaaa
 17 atggcggccgggttcaaaactgtggaaccgctggagtattacagg
    M  A  A  G  F  K  T  V  E  P  L  E  Y  Y  R
 62 agatttctgaaagaaaactgccgtccagatggaagagaacttggt
    R  F  L  K  E  N  C  R  P  D  G  R  E  L  G
107 gaattcagaaccacaactgtcaacataggttcgatcagtacagcg
    E  F  R  T  T  T  V  N  I  G  S  I  S  T  A
152 gatggctctgctctagtgaagctggggaacaccacagtcatttgt
    D  G  S  A  L  V  K  L  G  N  T  T  V  I  C
197 ggagttaaagcagaatttgcagcaccaccagtagatgcccctgat
    G  V  K  A  E  F  A  A  P  P  V  D  A  P  D
242 agaggatatgtcgtccctaatgtggacctaccaccgctgtgttca
    R  G  Y  V  V  P  N  V  D  L  P  P  L  C  S
287 tcgaggtttcggactggacctcctggagaagaggctcaagtaacc
    S  R  F  R  T  G  P  P  G  E  E  A  Q  V  T
332 agccagttcattgcagatgtcattgagaactcacacataattaag
    S  Q  F  I  A  D  V  I  E  N  S  H  I  I  K
377 aaagaggacttatgcatttctccagggaagcttgcttgggttcta
    K  E  D  L  C  I  S  P  G  K  L  A  W  V  L
422 tactgtgaccttatttgcctagactacgatgggaacattttggat
    Y  C  D  L  I  C  L  D  Y  D  G  N  I  L  D
467 gcctgcacatttgctttgttagcagctttaaagaatgtacagttg
    A  C  T  F  A  L  L  A  A  L  K  N  V  Q  L
512 cctgaagttactataaatgaagaaactgctttagcggaagtcaat
    P  E  V  T  I  N  E  E  T  A  L  A  E  V  N
557 ttaaagaagaaaagttatttgaatgttagagcaaacccagttgct
```